What is claimed is:

1. A solution comprising a tumor necrosis factor receptor 1 death domain (TNFR-1 DD).

2. The solution of Claim 1, wherein the TNFR-1 DD comprises amino acid residues 316-425 of Figure 6.

3. The solution of Claim 2, wherein the TNFR-1 DD is either unlabeled, ^{15}N enriched or ^{15}N,^{13}C enriched.

4. The solution of Claim 1, wherein the secondary structure of TNFR-1 DD comprises six alpha helices.

5. The solution of Claim 4, wherein α1 comprises amino acid residues A328-N336 of TNFR-1 DD, α2 comprises amino acid residues W342-L349 of TNFR-1 DD, α3 comprises amino acid residues P353-L361 of TNFR-1 DD, α4 comprises amino acid residues L367-R380 of TNFR-1 DD, α5 comprises amino acid residues L389-D398 of TNFR-1 DD and α6 comprises amino acid residues G403-L412 of TNFR-1 DD.

6. The solution of Claim 5, wherein TNFR-1 DD has the structure defined by the relative structural coordinates according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

7. An active site of a TRADD DD binding protein or peptide, wherein said active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues K343, E344, R347, R348 and

D353 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

8. An active site of a TRADD DD binding protein or peptide, wherein said active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues E369 and Y373 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

9. An active site of a TRADD DD binding protein or peptide, wherein said active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues E335, E386, E390, D398, E406, D407, E409 and E410 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

10. An active site of a TRADD DD binding protein or peptide, wherein said active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues R358, R365, R368, R379, R380, R381, R384, R385, R394 and R397 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

11. An agent which binds to the active site of Claim 7, wherein said agent is an inhibitor of TNFR-1 DD function.

12. An agent which binds to the active site of Claim 8, wherein said agent is an inhibitor of TNFR-1 DD function.

13. An agent which binds to the active site of Claim 9, wherein said agent is an inhibitor of TNFR-1 DD function.

14. An agent which binds to the active site of Claim 10, wherein said agent is an inhibitor of TNFR-1 DD function.

15. A method for identifying an agent that interacts with TNFR-1 DD, comprising the steps of:

(a) determining an active site of TNFR-1 DD from a three dimensional structure of TNFR-1 DD; and

(b) performing computer fitting analysis to identify an agent which interacts with said active site.

16. The method of Claim 15, wherein the active site is determined from the three dimensional structure defined by the structural coordinates set forth in Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

17. The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues K343, E344, R347, R348 and D353 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

18. The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues E369 and Y373 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

19. The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues E335, E386, E390, D398, E406, D407, E409 and E410 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

20. The method of Claim 15, wherein the active site is characterized by a three dimensional structure comprising the relative structural coordinates of amino acid residues R358, R365, R368, R379, R380, R381, R384, R385, R394 and R397 according to Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5 Å.

21. The method of Claim 15, further comprising contacting the identified agent with TNFR-1 DD in order to determine the effect the agent has on TNFR-1 DD.

22. The method of Claim 21, wherein the agent is an inhibitor of TNFR-1 DD.

23. The method of Claim 15, further comprising contacting the identified agent with TNFR-1 DD in the presence of a TNFR-1 DD binding molecule, and determining the effect the agent has on binding between TNFR-1 DD and the TNFR-1 DD binding molecule.

24. An agent identified by the method of Claim 15.

25. A method for identifying a potential inhibitor of TNFR-1 DD, comprising the steps of:

(a) generating a three dimensional model of TNFR-1 DD using the relative structural coordinates of the amino acids of Figure 8, ± a root mean square deviation from the conserved backbone atoms of said amino acids of not more than 1.5Å;

(b) employing said three-dimensional model to design or select a potential inhibitor; and

(c) synthesizing or obtaining said potential inhibitor.

26. The method according to Claim 25, wherein the potential inhibitor is designed *de novo*.

27. The method according to Claim 25, wherein the potential inhibitor is designed from a known inhibitor.

28. The method of Claim 25, further comprising contacting the potential inhibitor with TNFR-1 DD in order to determine the effect the inhibitor has on TNFR-1 DD.

29. The method of Claim 25, further comprising contacting the potential inhibitor with TNFR-1 DD in the presence of a TNFR-1 DD binding molecule, and determining the effect the potential inhibitor has on binding between TNFR-1 DD and the TNFR-1 DD binding molecule.

30. The method according to Claim 25, wherein the step of employing the three dimensional structure to design or select the potential inhibitor comprises the steps of:

(a) identifying chemical entities or fragments capable of associating with TNFR-1 DD; and

(b) assembling the identified chemical entities or fragments into a single molecule to provide the structure of the potential inhibitor.

31. The method according to Claim 30, wherein the potential inhibitor is designed *de novo*.

32. The method according to Claim 30, wherein the potential inhibitor is designed from a known inhibitor.

33. The method of Claim 30, further comprising contacting the potential inhibitor with TNFR-1 DD in order to determine the effect the inhibitor has on TNFR-1 DD.

34. The method of Claim 30, further comprising contacting the potential inhibitor with TNFR-1 DD in the presence of a TNFR-1 DD binding molecule, and determining the effect the potential inhibitor has on binding between TNFR-1 DD and the TNFR-1 DD binding molecule.

35. An inhibitor identified or designed by the method of Claim 25.

36. An inhibitor identified or designed by the method of Claim 30.